

SEQUENCE LISTING

<110> Ruben et al.

<120> Human Tumor Necrosis Factor Receptor TR17

<130> PF524P1

<140> Unassigned

<141> 2001-09-25

<150> 60/254,874

<151> 2000-12-13

<150> 60/235,991

<151> 2000-09-26

<150> 09/533,822

<151> 2000-03-24

<150> 60/188,208

<151> 2000-03-10

<160> 7

<170> PatentIn Ver. 2.1

<210> 1

<211> 882

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (1)..(882)

<400> 1

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Met Ser Gly Leu Gly Arg Ser Arg Arg Gly Arg Ser Arg Val Asp
1 5 10 15

cag gag gag cgc ttt cca cag ggc ctg tgg acg ggg gtg gct atg aga
Gln Glu Glu Arg Phe Pro Gln Gly Leu Trp Thr Gly Val Ala Met Arg
20 25 30

tcc tgc ccc gaa gag cag tac tgg gat cct ctg ctg ggt acc tgc atg
Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu Gly Thr Cys Met
35 40 45

tcc tgc aaa acc att tgc aac cat cag agc cag cgc acc tgt gca gcc
Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg Thr Cys Ala Ala
50 55 60

ttc tgc agg tca ctc agc tgc cgc aag gag caa ggc aag ttc tat gac
Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe Tyr Asp
65 70 75 80

cat ctc ctg agg gac tgc atc agc tgt gcc tcc atc tgt gga cag cac
His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His
85 90 95

cct aag caa tgt gca tac ttc tgt gag aac aag ctc agg agc cca gtg Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser Pro Val 100 105 110	336
aac ctt cca cca gag ctc agg aga cag cgg agt gga gaa gtt gaa aac Asn Leu Pro Pro Glu Leu Arg Arg Gln Arg Ser Gly Glu Val Glu Asn 115 120 125	384
aat tca gac aac tcg gga agg tac caa gga ttg gag cac aga ggc tca Asn Ser Asp Asn Ser Gly Arg Tyr Gln Gly Leu Glu His Arg Gly Ser 130 135 140	432
gaa gca agt cca gct ctc ccg ggg ctg aag ctg agt gca gat cag gtg Glu Ala Ser Pro Ala Leu Pro Gly Leu Lys Leu Ser Ala Asp Gln Val 145 150 155 160	480
gcc ctg gtc tac agc acg ctg ggg ctc tgc ctg tgt gcc gtc ctc tgc Ala Leu Val Tyr Ser Thr Leu Gly Leu Cys Leu Cys Ala Val Leu Cys 165 170 175	528
tgc ttc ctg gtg gcg gtg gcc tgc ttc ctc aag aag agg ggg gat ccc Cys Phe Leu Val Ala Val Ala Cys Phe Leu Lys Lys Arg Gly Asp Pro 180 185 190	576
tgc tcc tgc cag ccc cgc tca agg ccc cgt caa agt ccg gcc aag tct Cys Ser Cys Gln Pro Arg Ser Arg Pro Arg Gln Ser Pro Ala Lys Ser 195 200 205	624
tcc cag gat cac gcg atg gaa gcc ggc agc cct gtg agc aca tcc ccc Ser Gln Asp His Ala Met Glu Ala Gly Ser Pro Val Ser Thr Ser Pro 210 215 220	672
gag cca gtg gag acc tgc agc ttc tgc ttc cct gag tgc agg gcg ccc Glu Pro Val Glu Thr Cys Ser Phe Cys Phe Pro Glu Cys Arg Ala Pro 225 230 235 240	720
acg cag gag agc gca gtc acg cct ggg acc ccc gac ccc act tgt gct Thr Gln Glu Ser Ala Val Thr Pro Gly Thr Pro Asp Pro Thr Cys Ala 245 250 255	768
gga agg tgg ggg tgc cac acc agg acc aca gtc ctg cag cct tgc cca Gly Arg Trp Gly Cys His Thr Arg Thr Thr Val Leu Gln Pro Cys Pro 260 265 270	816
cac atc cca gac agt ggc ctt ggc att gtg tgt gtg cct gcc cag gag His Ile Pro Asp Ser Gly Leu Gly Ile Val Cys Val Pro Ala Gln Glu 275 280 285	864
ggg ggc cca ggt gca taa Gly Gly Pro Gly Ala 290	882

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<213> Homo sapiens

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Met Ser Gly Leu Gly Arg Ser Arg Arg Gly Gly Arg Ser Arg Val Asp
 1 5 10 15
 Gln Glu Glu Arg Phe Pro Gln Gly Leu Trp Thr Gly Val Ala Met Arg
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 Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu Gly Thr Cys Met
 35 40 45
 Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg Thr Cys Ala Ala
 50 55 60
 Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe Tyr Asp
 65 70 75 80
 His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His
 85 90 95
 Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser Pro Val
 100 105 110
 Asn Leu Pro Pro Glu Leu Arg Arg Gln Arg Ser Gly Glu Val Glu Asn
 115 120 125
 Asn Ser Asp Asn Ser Gly Arg Tyr Gln Gly Leu Glu His Arg Gly Ser
 130 135 140
 Glu Ala Ser Pro Ala Leu Pro Gly Leu Lys Leu Ser Ala Asp Gln Val
 145 150 155 160
 Ala Leu Val Tyr Ser Thr Leu Gly Leu Cys Leu Cys Ala Val Leu Cys
 165 170 175
 Cys Phe Leu Val Ala Val Ala Cys Phe Leu Lys Lys Arg Gly Asp Pro
 180 185 190
 Cys Ser Cys Gln Pro Arg Ser Arg Pro Arg Gln Ser Pro Ala Lys Ser
 195 200 205
 Ser Gln Asp His Ala Met Glu Ala Gly Ser Pro Val Ser Thr Ser Pro
 210 215 220
 Glu Pro Val Glu Thr Cys Ser Phe Cys Phe Pro Glu Cys Arg Ala Pro
 225 230 235 240
 Thr Gln Glu Ser Ala Val Thr Pro Gly Thr Pro Asp Pro Thr Cys Ala
 245 250 255
 Gly Arg Trp Gly Cys His Thr Arg Thr Thr Val Leu Gln Pro Cys Pro
 260 265 270
 His Ile Pro Asp Ser Gly Leu Gly Ile Val Cys Val Pro Ala Gln Glu
 275 280 285
 Gly Gly Pro Gly Ala
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 tctcccgac tcctgaggc acatgcgtgg tggtggacgt aagccacgaa gaccctgagg 180
 tcaagttcaa ctggtagctg gacggcgtgg aggtgcataa tgccaagaca aagccgcggg 240
 aggagcagta caacagcagc taccgtgtgg tcagcgtcct caccgtcctg caccaggact 300
 ggctgaatgg caaggagtac aagtgcagg tctccaacaa agccctccca acccccattg 360
 agaaaaaccat ctccaaagcc aaaggccagc cccgagaacc acaggtgtac accctgcccc 420
 catcccgga ttagctgacc aagaaccagg tcagcctgac ctgcctggc aaaggcttot 480
 atccaagcga catcgccgtg gagtgggaga gcaatgggca gccggagaac aactacaaga 540
 ccacgcctcc cgtgctggac tccgacggct ccttcttcct ctacagcaag ctcaccgtgg 600
 acaagagcag gtggcagcag gggAACGTCT tctcatgctc cgtgatgcat gaggctctgc 660
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<210> 4
<211> 9
<212> PRT
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<220>
<221> SITE
<222> (1) .. (5)
<223> Xaa equal any amino acid

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<223> Xaa equal any amino acid

<400> 4
Xaa Xaa Xaa Xaa Xaa Glu Gly Ser Xaa
1 5

<210> 5
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<212> PRT
<213> Homo sapiens

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<212> PRT
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1 5 10 15

Ala

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<212> PRT
<213> Artificial Sequence

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<222> (1) .. (22)
<223> consensus signal sequence

<400> 7

Met Pro Thr Trp Ala Trp Trp Leu Phe Leu Val Leu Leu Leu Ala Leu
1 5 10 15

Trp Ala Pro Ala Arg Gly
20